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RAW SEQUENCE LISTING DATE: 03/28/2002
PATENT APPLICATION: US/09/980,585A TIME: 10:45:19

Input Set : N:\Crf3\03212002\I980585.raw
Output Set: N:\CRF3\03282002\I980585A.raw

1 <110> APPLICANT: LILIU, Esa-Matti
2 VIRTA, Marko
3 <120> TITLE OF INVENTION: A Method to Enable Assessment of Growth and Death of Micro-organisms
4 <130> FILE REFERENCE: 2328-124
5 <140> CURRENT APPLICATION NUMBER: US/09/980,585A
C--> 6 <141> CURRENT FILING DATE: 2000-06-07
7 <150> PRIOR APPLICATION NUMBER: PCT/FI00/00507
8 <151> PRIOR FILING DATE: 2000-06-07
9 <150> PRIOR APPLICATION NUMBER: FI 991296
10 <151> PRIOR FILING DATE: 1999-06-07
11 <160> NUMBER OF SEQ ID NOS: 4
12 <170> SOFTWARE: PatentIn version 3.0
14 <210> SEQ ID NO: 1
15 <211> LENGTH: 5051
16 <212> TYPE: DNA
17 <213> ORGANISM: Artificial Sequence
18 <220> FEATURE:
19 <223> OTHER INFORMATION: pGFP+Luc* plasmid
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24 <222> LOCATION: (289)..(1005)
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31 <223> OTHER INFORMATION: coding sequence for beta-lactamase
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35 tcactcatta ggcaccccaag gctttacact ttatgtttcc ggctcgtatg ttgtgtggaa 180
36 ttgtgagcgg ataacaattt cacacagggaa acagctatga ccattgattac gccaagcttg 240
37 catgcctgca ggtcgactct agaggatccc cgggtaccgg tcgcccaccat ggtgagcaag 300
38 ggcgaggagc tggtcaccgg ggttgtgccc atcctggtc agctggacgg cgacgtaaac 360
39 ggccacaagt tcagcgtgtc cggcgagggc gagggcgtatg coacctacgg caagctgacc 420
40 ctgaagttca tctgcaccac cggcaagctg cccgtgccct ggcccaccct cgtgaccacc 480
41 ctgacctacg gcgtgcagtg cttcagccgc taccccgacc acatgaagca gcacgacttc 540
42 ttcaagtccg ccatgcccga aggctacgtc caggagcgc当地 ccattttctt caaggacgac 600
43 ggcaactaca agaccgc当地 cgaggtgaag ttcgaggccg acaccctggt gaaccgc当地 660
44 gagctgaagg gcatcgactt caaggaggac ggcaacatcc tggggcacaa gctggagttac 720

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45	aactacaaca	gccacaacgt	ctatatcatg	gccgacaaggc	agaagaacgg	catcaaggtg	780
46	aacttcaaga	tccgcaccaa	catcgaggac	ggcagcgtgc	agctcgccga	ccactaccag	840
47	cagaacaccc	ccatcgccga	cgccccctg	ctgctgccc	acaaccacta	cctgagcacc	900
48	cagtccgccc	tgagcaaaga	ccccaaacgg	aagcgcgatc	acatggtcct	gctggagttc	960
49	gtgaccgccc	ccgggatcac	tctcgccatg	gacgagctgt	acaagtaaag	cggccgctct	1020
50	agaacttagt	gatccccctg	accatggaaag	acgccaaaaa	cataaagaaaa	ggccggcgc	1080
51	cattctatcc	gctagaggat	ggaaccgctg	gagagcaact	gcataaggct	atgaagagat	1140
52	acgccttgtt	tcctggaaaca	attgccttta	cagatgcaca	tatcgaggtg	aacatcacgt	1200
53	acgcgaaata	cttcgaaatg	tccgttcggt	tggcagaagc	tatgaaacga	tatggctga	1260
54	atacaatca	cagaatcgctc	gtatgcagt	aaaactctct	tcaattctt	atgcccgtgt	1320
55	tggcgcggtt	atttatcgga	gttgcagttt	cgcccgcgaa	cgacatttat	aatgaacgtg	1380
56	aattgctcaa	cagtatgaac	atttcgcage	ctaccgtatgt	gtttgtttcc	aaaaaggggt	1440
57	tgcaaaaaat	tttgaacgt	caaaaaaaaaat	taccaataat	ccagaaaaatt	attatcatgg	1500
58	attctaaaac	ggattaccag	ggatttcagt	cgatgtacac	gttcgtcaca	tctcatctac	1560
59	ctcccggtt	taatgaatac	gattttgtac	cagagtccctt	tgatcggtac	aaaacaattt	1620
60	caactgataat	gaactccct	ggatctactg	ggttaccaa	gggtgtggcc	cttccgcata	1680
61	gaactgcctg	cgtcagattc	tcgcatgcca	gagatccat	tttggcaat	caaatcatc	1740
62	cggatactgc	gattttaagt	gttgttccat	tccatcacgg	tttggaaatg	tttactacac	1800
63	tcggatattt	gatatgttga	tttcgagtcg	tcttaatgt	tagatttga	gaagagctgt	1860
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65	cattcttcgc	caaaaagcaact	ctgattgaca	aatacgtattt	atctaatttta	cacgaaattt	1980
66	cttctggggg	cgcaccttctt	tcgaaagaag	tcgggaaagc	ggttgaaaaa	cgcttccatc	2040
67	ttccaggggat	acgacaagga	tatgggctca	ctgagactac	atcagctattt	ctgattacac	2100
68	ccgaggggg	tgataaaaccg	ggcgcgggtcg	gtaaagttgt	tccatttttt	gaagcgaagg	2160
69	ttgtggatct	ggataccggg	aaaacgctgg	gcgttaatca	gagaggcgaa	ttatgtgtca	2220
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71	acaaggatgg	atggctacat	tctggagaca	tagcttactg	ggacgaagac	gaacacttct	2340
72	tcatagttga	ccgcttgaag	tcttaatttta	aatacaaaagg	ataccaggt	gcccccgctg	2400
73	aattggagtc	gatattgtt	caacacccca	acatctcga	cgccggcggt	gcaggtcttc	2460
74	ccgacgatga	cgccgggtgaa	cttccgcgg	ccgttgggt	tttggagcac	ggaaagacga	2520
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76	gcggaggagt	tgtgtttgt	gacgaagttac	cgaaaggct	taccggaaaa	ctcgacgca	2640
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78	taactgtatt	cagcgatgac	gaaattctt	gctattgtaa	tactctagg	gtcgaggaa	2760
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81	ctgttaagcg	atgccccgg	cagacaagcc	cgtcagggg	cgtcagcgg	tgttggcggg	2940
82	tgtcgccgt	ggcttaacta	tgccggatca	gagcagattt	tacttaggt	gcaccatatg	3000
83	cggtgtgaaa	taccgcacag	atgcgttaagg	agaaaatacc	gcatcaggcg	gccttaaggg	3060
84	cctctgtata	cgccttatttt	tataaggtaa	tgtcatgata	ataatggttt	cttagacgtc	3120
85	agggtggcact	tttcggggaa	atgtgcgcgg	aaccctattt	tgtttatttt	tctaaataca	3180
86	ttcaaatatg	tatccgtca	ttagacaata	accctgataa	atgcctcaat	aatattgaaa	3240
87	aaggaagagt	atgagtattt	aacatttccg	tgtcgccctt	attccctttt	ttgcggcatt	3300
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89	gttgggtgca	cgagtgggtt	acatcgaaact	ggatctcaac	agcggtaa	tccttgagag	3420
90	tttcgcccc	gaagaacgtt	ttccaaatgt	gagcactttt	aaagttctgc	tatgtggcgc	3480
91	ggtattatcc	cgtattgacg	ccgggcaaga	gcaactcggt	cgccgcatac	actattctca	3540
92	gaatgactt	gttggactt	caccagtcac	agaaaagcat	cttacggat	gcatgacagt	3600
93	aagagaatta	tgcagtgt	ccataaccat	gagtgataac	actgcggcca	acttacttct	3660

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94	gacaacgatc ggaggaccga aggagctaac cgctttttg cacaacatgg gggatcatgt	3720
95	aactcgccctt gatcggttggg aaccggagct gaatgaagcc ataccaaactg acgagcgtga	3780
96	caccacgatg cctgttagcaa tggcaacaac gttgcgc当地 ctattaactg gcgaactact	3840
97	tactcttagct tccccggcaac aattaataga ctggatggag gcccataaag ttgcaggacc	3900
98	acttctgcgc tcggcccttc cggctggctg gtttattgct gataaatctg gagccgggtga	3960
99	gcgtgggtct cgcgttatca ttgcagcaact gggccagat ggttaaggccct cccgtatcg	4020
100	agtatctac acgacgggga gtcaggcaac tatggatgaa cgaaaatagac agatcgctga	4080
101	gataggtgcc tcactgatta agcattggta actgtcagac caagtttact catataact	4140
102	tttagattgat taaaacttc atttttaatt taaaaggatc taggtgaaga tccttttga	4200
103	taatctcatg accaaaatcc cttAACGTGA gtttctgtc cactgagcgt cagacccgt	4260
104	agaaaagatc aaaggatctt cttgagatcc ttttttctg cgcgtatct gctgcttgca	4320
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113	cggtttcgc cacctctgac ttgagcgtog attttgtga tgctcgtcag gggggcggag	4860
114	cctatggaaa aacgcccagca acgcggcctt ttacggttc ctggccttt gctggcctt	4920
115	tgcacatg ttctttctgt cgttatcccc tgattctgt gataaccgtt ttacggcctt	4980
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123 <220> FEATURE:

124 <223> OTHER INFORMATION: source of GFP unknown

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129	20 25 30	
130	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
131	35 40 45	
132	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
133	50 55 60	
134	Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
135	65 70 75 80	
136	Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
137	85 90 95	
138	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
139	100 105 110	
140	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
141	115 120 125	
142	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
143	130 135 140	

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144 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 146 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 147 165 170 175
 148 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 149 180 185 190
 150 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 151 195 200 205
 152 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 153 210 215 220
 154 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 155 225 230 235
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 159 <212> TYPE: PRT
 160 <213> ORGANISM: Unknown
 161 <220> FEATURE:
 162 <223> OTHER INFORMATION: source of firefly luciferase unknown
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 166 Leu Glu Asp Gly Thr Ala Gly Glu Gln Leu His Lys Ala Met Lys Arg
 167 20 25 30
 168 Tyr Ala Leu Val Pro Gly Thr Ile Ala Phe Thr Asp Ala His Ile Glu
 169 35 40 45
 170 Val Asn Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val Arg Leu Ala
 171 50 55 60
 172 Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg Ile Val Val
 173 65 70 75 80
 174 Cys Ser Glu Asn Ser Leu Gln Phe Phe Met Pro Val Leu Gly Ala Leu
 175 85 90 95
 176 Phe Ile Gly Val Ala Val Ala Pro Ala Asn Asp Ile Tyr Asn Glu Arg
 177 100 105 110
 178 Glu Leu Leu Asn Ser Met Asn Ile Ser Gln Pro Thr Val Val Phe Val
 179 115 120 125
 180 Ser Lys Lys Gly Leu Gln Lys Ile Leu Asn Val Gln Lys Lys Leu Pro
 181 130 135 140
 182 Ile Ile Gln Lys Ile Ile Met Asp Ser Lys Thr Asp Tyr Gln Gly
 183 145 150 155 160
 184 Phe Gln Ser Met Tyr Thr Phe Val Thr Ser His Leu Pro Pro Gly Phe
 185 165 170 175
 186 Asn Glu Tyr Asp Phe Val Pro Glu Ser Phe Asp Arg Asp Lys Thr Ile
 187 180 185 190
 188 Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys Gly Val
 189 195 200 205
 190 Ala Leu Pro His Arg Thr Ala Cys Val Arg Phe Ser His Ala Arg Asp
 191 210 215 220
 192 Pro Ile Phe Gly Asn Gln Ile Ile Pro Asp Thr Ala Ile Leu Ser Val
 193 225 230 235 240

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194 Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly Tyr Leu
 195 245 250 255
 196 Ile Cys Gly Phe Arg Val Val Leu Met Tyr Arg Phe Glu Glu Leu
 197 260 265 270
 198 Phe Leu Arg Ser Leu Gln Asp Tyr Lys Ile Gln Ser Ala Leu Leu Val
 199 275 280 285
 200 Pro Thr Leu Phe Ser Phe Phe Ala Lys Ser Thr Leu Ile Asp Lys Tyr
 201 290 295 300
 202 Asp Leu Ser Asn Leu His Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser
 203 305 310 315 320
 204 Lys Glu Val Gly Glu Ala Val Ala Lys Arg Phe His Leu Pro Gly Ile
 205 325 330 335
 206 Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Leu Ile Thr
 207 340 345 350
 208 Pro Glu Gly Asp Asp Lys Pro Gly Ala Val Gly Lys Val Val Pro Phe
 209 355 360 365
 210 Phe Glu Ala Lys Val Val Asp Leu Asp Thr Gly Lys Thr Leu Gly Val
 211 370 375 380
 212 Asn Gln Arg Gly Glu Leu Cys Val Arg Gly Pro Met Ile Met Ser Gly
 213 385 390 395 400
 214 Tyr Val Asn Asn Pro Glu Ala Thr Asn Ala Leu Ile Asp Lys Asp Gly
 215 405 410 415
 216 Trp Leu His Ser Gly Asp Ile Ala Tyr Trp Asp Glu Asp Glu His Phe
 217 420 425 430
 218 Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln
 219 435 440 445
 220 Val Ala Pro Ala Glu Leu Glu Ser Ile Leu Leu Gln His Pro Asn Ile
 221 450 455 460
 222 Phe Asp Ala Gly Val Ala Gly Leu Pro Asp Asp Asp Ala Gly Glu Leu
 223 465 470 475 480
 224 Pro Ala Ala Val Val Val Leu Glu His Gly Lys Thr Met Thr Glu Lys
 225 485 490 495
 226 Glu Ile Val Asp Tyr Val Ala Ser Gln Val Thr Thr Ala Lys Lys Leu
 227 500 505 510
 228 Arg Gly Gly Val Val Phe Val Asp Glu Val Pro Lys Gly Leu Thr Gly
 229 515 520 525
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 238 <213> ORGANISM: Unknown
 239 <220> FEATURE:
 240 <223> OTHER INFORMATION: source of beta-lactamase unknown
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